

What is claimed is:

1. A substantially purified polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-6, and fragments thereof.
- 5 2. A substantially purified variant having at least 90% amino acid sequence identity to the amino acid sequence of claim 1.
3. An isolated and purified polynucleotide encoding the polypeptide of claim 1.
- 10 4. An isolated and purified polynucleotide variant having at least 70% polynucleotide sequence identity to the polynucleotide of claim 3.
5. An isolated and purified polynucleotide which hybridizes under stringent conditions to  
15 the polynucleotide of claim 3.
6. An isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide of claim 3.
- 20 7. A method for detecting a polynucleotide, the method comprising the steps of:
  - (a) hybridizing the polynucleotide of claim 6 to at least one nucleic acid in a sample, thereby forming a hybridization complex; and
  - (b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of the polynucleotide in the sample.
- 25 8. The method of claim 7 further comprising amplifying the polynucleotide prior to hybridization.
9. An isolated and purified polynucleotide comprising a polynucleotide sequence selected  
30 from the group consisting of SEQ ID NO:7-12, and fragments thereof.
10. An isolated and purified polynucleotide variant having at least 70% polynucleotide sequence identity to the polynucleotide of claim 9.
- 35 11. An isolated and purified polynucleotide having a sequence which is complementary to the

polynucleotide of claim 9.

12. An expression vector comprising at least a fragment of the polynucleotide of claim 3.
- 5 13. A host cell comprising the expression vector of claim 12.
14. A method for producing a polypeptide, the method comprising the steps of:
  - a) culturing the host cell of claim 13 under conditions suitable for the expression of the polypeptide; and
  - 10 b) recovering the polypeptide from the host cell culture.
15. A pharmaceutical composition comprising the polypeptide of claim 1 in conjunction with a suitable pharmaceutical carrier.
- 15 16. A purified antibody which specifically binds to the polypeptide of claim 1.
17. A purified agonist of the polypeptide of claim 1.
18. A purified antagonist of the polypeptide of claim 1.
- 20 19. A method for treating or preventing a disorder associated with decreased expression or activity of HCHP, the method comprising administering to a subject in need of such treatment an effective amount of the pharmaceutical composition of claim 15.
- 25 20. A method for treating or preventing a disorder associated with increased expression or activity of HCHP, the method comprising administering to a subject in need of such treatment an effective amount of the antagonist of claim 18.

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1	M A A A L R S G W C R C P R R C L G S G I Q F L S S H N L P H G S T	1556139
1	M A A A R L R G G W C R C P R R C L G S G I Q F L S S H N L P H G S S	g2351410
36	Y Q M R R P G G E L P L S K S Y S S G N R K G F L S G L L D N V K Q E	1556139
36	Y Q I S R P G R E L T L T K S Y S S G S R K G F L S G L L D N I K Q E	g2351410
71	L A K N K E M K E S I K K F R D E A R R L E E S D V L Q E A R R K Y K	1556139
71	L A K N K E M K E S I K K F R D E A K K L E E S D A L Q E A R R K Y K	g2351410
106	T I E S E T V R T S E V L R K K L G E L T G T V K E S L H E V S K S D	1556139
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211	T E F A G A K F K E S K V F E A N E E A L G V V L H K D S K W Y Q Q W	g2351410
246	K D F K E N N V V F N R F F E M K K Y D E S D N A F I R A S R A L T	1556139
246	K D F K D N N V V F N R F F E M K K Y D E S D N V L I R A S R A L T	g2351410

FIGURE 1A

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281	DKVTDL	LGGLF	SKT	EMSEV	L	T	E	I	L	R	V	D	P	A	F	D	K	D	R	F	1556139													
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316	LKQCE	N	D	I	I	P	N	V	L	E	A	M	I	S	G	E	L	D	I	L	K	D	W	C	Y	E	A	T	Y	S	Q	1556139		
316	LHQCE	T	D	I	I	P	N	I	L	E	A	M	I	S	G	E	L	D	I	L	K	D	W	C	Y	E	A	T	Y	S	Q	g2351410		
351	LAHP	I	Q	Q	A	K	A	L	G	L	Q	F	H	S	R	I	L	D	I	D	N	V	D	L	A	M	G	K	M	M	E	Q	1556139	
351	LAHP	I	Q	Q	A	K	A	L	G	F	Q	F	H	S	R	I	L	D	I	S	N	V	D	L	A	M	G	K	M	M	E	Q	g2351410	
386	GPV	L	I	I	T	F	Q	A	Q	L	V	M	V	R	N	P	K	G	E	V	V	E	G	D	P	D	K	V	L	R	M	L	1556139	
386	GPV	L	I	V	T	F	Q	A	Q	V	V	M	V	I	K	N	S	K	G	E	V	Y	D	G	D	P	D	K	V	Q	R	M	L	g2351410
421	YVW	A	L	C	R	D	Q	D	E	L	N	P	Y	A	A	W	R	L	L	D	I	S	A	S	S	T	E	Q	I	L			1556139	
421	YVW	A	L	C	R	D	Q	E	E	L	N	P	Y	A	A	W	R	L	L	D	I	S	A	S	S	T	E	Q	I	L			g2351410	

FIGURE 1B

1	M	A	V	R	S	L	W	A	G	R	L	R	V	Q	R	L	L	A	W	S	A	A	W	E	S	K	G	W	P	L	3658451
1	-	A	A	R	S	L	W	A	V	Q	-	R	L	Q	R	L	L	A	S	G	A	M	S	E	S	R	G	W	L	H	g3411072
31	P	F	S	T	A	T	Q	R	T	A	G	E	D	C	R	S	E	D	P	P	D	E	L	G	P	P	L	A	E	R	3658451
29	P	F	S	T	A	T	Q	R	T	A	G	E	D	C	S	S	E	D	P	P	D	G	L	G	P	S	L	A	E	Q	g3411072
61	A	L	R	V	K	A	V	K	L	E	K	E	V	Q	D	L	T	V	R	Y	Q	R	A	I	A	D	C	E	N	I	3658451
59	A	L	R	L	K	A	V	K	L	E	K	E	V	Q	D	L	T	L	R	Y	Q	R	A	V	A	D	C	E	N	I	g3411072
91	R	R	R	T	Q	R	C	V	E	D	A	K	I	F	G	I	Q	S	F	C	K	D	L	V	E	V	A	D	I	L	3658451
89	R	R	R	T	Q	R	C	V	E	D	A	K	I	F	G	I	Q	S	F	C	K	D	L	V	E	V	A	D	I	L	g3411072
121	E	K	T	E	C	I	S	E	E	S	E	P	E	D	Q	K	L	T	L	E	K	V	F	R	G	L	L	L	L	3658451	
119	E	K	T	A	K	C	S	E	G	A	E	P	E	D	H	R	R	T	L	E	K	V	F	Q	G	L	S	L	L	g3411072	
151	E	A	K	L	K	S	V	F	A	K	H	G	L	E	K	L	T	P	I	G	D	K	Y	D	P	H	E	H	E	L	3658451
149	E	A	R	L	K	S	V	F	T	K	H	G	L	E	K	M	T	P	I	G	D	K	Y	D	P	H	E	H	E	L	g3411072
181	I	C	H	V	P	A	G	V	G	V	Q	P	G	T	V	A	L	V	R	Q	D	G	Y	K	L	H	G	R	T	I	3658451
179	I	C	H	M	P	A	G	V	G	V	Q	P	G	T	V	A	L	V	R	Q	D	G	Y	K	L	H	G	R	T	I	g3411072
211	R	L	A	R	V	E	V	A	V	E	S	Q	R	R	L	3658451															
209	R	L	A	Q	V	E	V	A	V	E	S	Q	R	R	L	g3411072															

FIGURE 2

1	M	G	K	D	Y	Y	C	I	L	G	I	E	K	G	A	S	D	E	D	I	K	K	A	Y	R	K	Q	A	L	K	4217610	
1	M	G	K	D	Y	Y	Q	T	L	G	L	A	R	G	A	S	D	E	E	I	K	R	A	Y	R	Q	A	L	R	g1816452		
31	F	H	P	D	K	N	K	S	P	Q	A	E	E	K	F	K	E	V	A	E	A	Y	E	V	L	S	D	P	K	K	4217610	
31	Y	H	P	D	K	N	K	E	P	G	A	E	E	K	F	K	E	I	A	E	A	Y	D	V	L	S	D	P	R	K	g1816452	
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87	R	Y	T	F	H	G	D	P	H	A	T	F	A	A	F	F	G	G	S	N	P	F	E	I	F	F	G	R	R	M	4217610	
91	S	Y	T	F	H	G	D	P	H	A	M	F	A	E	F	F	G	G	R	N	P	F	D	T	F	F	G	Q	R	N	g1816452	
117	G	G	G	R	D	S	E	E	M	E	I	D	G	D	P	F	S	A	F	G	F	S	M	N	G	Y	P	-	-	-	4217610	
121	G	E	-	-	-	E	G	M	D	I	D	-	D	P	F	S	G	F	P	M	G	M	G	G	F	T	N	V	N	g1816452		
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146	F	G	R	S	R	S	A	Q	E	P	A	R	K	K	Q	D	P	P	V	T	H	D	L	R	V	S	L	E	E	I	g1816452	
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176	Y	S	G	C	T	K	K	M	K	I	S	H	K	R	L	N	P	D	G	K	S	I	R	N	E	D	K	I	L	T	g1816452	
202	I	E	I	K	K	G	W	K	E	G	T	K	I	T	F	P	R	E	G	D	E	T	P	N	S	I	P	A	D	I	4217610	
206	I	E	V	K	K	G	W	K	E	G	T	K	I	T	F	P	K	E	G	D	Q	T	S	N	I	P	A	D	I	g1816452		

FIGURE 3A

232 V F I I K D K D H P K F K R D G S N I I Y T A K I S L R E A 4217610  
236 V F V L K D K P H N I F K R D G S D V I Y P A R I S L R E A g1816452

262 L C G C S I N V P T L D G R N I P M S V N D I V K P G M R R 4217610  
266 L C G C T V N V P T L D G R T I P V V F K D V I R P G M R R g1816452

292 R I I G Y G L P F P K K S 4217610  
296 K V P G E G L P L P K T P E K R G D L I I E F E V I F P E R g1816452

304 4217610  
326 I P Q T S R T V L E Q V L P I g1816452

FIGURE 3B

## SEQUENCE LISTING

&lt;110&gt; INCYTE PHARMACEUTICALS, INC.

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HILLMAN, Jennifer L.

YUE, Henry

PATTERSON, Chandra

BAUGHN, Mariah R.

BATRA, Sajeev

&lt;120&gt; HUMAN CHAPERONE PROTEINS

&lt;130&gt; PF-0595 PCT

&lt;140&gt; To Be Assigned

&lt;141&gt; Herewith

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1999-04-19

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Pro	His	Gly	Ser	Thr	Tyr	Gln	Met	Arg	Arg	Pro	Gly	Gly	Glu	Leu
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Pro	Leu	Ser	Lys	Ser	Tyr	Ser	Ser	Gly	Asn	Arg	Lys	Gly	Phe	Leu
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Glu	Met	Lys	Glu	Ser	Ile	Lys	Lys	Phe	Arg	Asp	Glu	Ala	Arg	Arg
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Leu	Glu	Glu	Ser	Asp	Val	Leu	Gln	Glu	Ala	Arg	Arg	Lys	Tyr	Lys
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Thr	Ile	Glu	Ser	Glu	Thr	Val	Arg	Thr	Ser	Glu	Val	Leu	Arg	Lys
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Lys	Leu	Gly	Glu	Leu	Thr	Gly	Thr	Val	Lys	Glu	Ser	Leu	His	Glu
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Val Ser Lys Ser Asp Leu Gly Arg Lys Ile Lys Glu Gly Val Glu	140	145	150
Glu Ala Ala Lys Thr Ala Lys Gln Ser Ala Glu Ser Val Ser Lys	155	160	165
Gly Gly Glu Lys Leu Gly Arg Thr Ala Ala Phe Arg Ala Leu Ser	170	175	180
Gln Gly Val Glu Ser Val Lys Lys Glu Ile Asp Asp Ser Val Leu	185	190	195
Gly Gln Thr Gly Pro Tyr Arg Arg Pro Gln Arg Leu Arg Lys Arg	200	205	210
Thr Glu Phe Ala Gly Asp Lys Phe Lys Glu Glu Lys Val Phe Glu	215	220	225
Pro Asn Glu Glu Ala Leu Gly Val Val Leu His Lys Asp Ser Lys	230	235	240
Trp Tyr Gln Gln Trp Lys Asp Phe Lys Glu Asn Asn Val Val Phe	245	250	255
Asn Arg Phe Phe Glu Met Lys Met Lys Tyr Asp Glu Ser Asp Asn	260	265	270
Ala Phe Ile Arg Ala Ser Arg Ala Leu Thr Asp Lys Val Thr Asp	275	280	285
Leu Leu Gly Gly Leu Phe Ser Lys Thr Glu Met Ser Glu Val Leu	290	295	300
Thr Glu Ile Leu Arg Val Asp Pro Ala Phe Asp Lys Asp Arg Phe	305	310	315
Leu Lys Gln Cys Glu Asn Asp Ile Ile Pro Asn Val Leu Glu Ala	320	325	330
Met Ile Ser Gly Glu Leu Asp Ile Leu Lys Asp Trp Cys Tyr Glu	335	340	345
Ala Thr Tyr Ser Gln Leu Ala His Pro Ile Gln Gln Ala Lys Ala	350	355	360
Leu Gly Leu Gln Phe His Ser Arg Ile Leu Asp Ile Asp Asn Val	365	370	375
Asp Leu Ala Met Gly Lys Met Met Glu Gln Gly Pro Val Leu Ile	380	385	390
Ile Thr Phe Gln Ala Gln Leu Val Met Val Val Arg Asn Pro Lys	395	400	405
Gly Glu Val Val Glu Gly Asp Pro Asp Lys Val Leu Arg Met Leu	410	415	420
Tyr Val Trp Ala Leu Cys Arg Asp Gln Asp Glu Leu Asn Pro Tyr	425	430	435
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Ala	Ser	Asp	Glu	Asp	Leu	Lys	Lys	Ala	Tyr	Arg	Arg	Leu	Ala	Leu	125	130	135	
Lys	Phe	His	Pro	Asp	Lys	Asn	His	Ala	Pro	Gly	Ala	Thr	Glu	Ala	140	145	150	
Phe	Lys	Ala	Ile	Gly	Thr	Ala	Tyr	Ala	Val	Leu	Ser	Asn	Pro	Glu	155	160	165	
Lys	Arg	Lys	Gln	Tyr	Asp	Gln	Phe	Gly	Asp	Asp	Lys	Ser	Gln	Ala	170	175	180	
Ala	Arg	His	Gly	His	Gly	His	Gly	Asp	Phe	His	Arg	Gly	Phe	Glu	185	190	195	
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Arg	Tyr	Thr	Tyr	Gln	Gln	Arg	Gln	Asp	Arg	Arg	Asp	Asn	Gln	Gly	230	235	240	
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Arg	Val	Thr	Asp	His	Leu	Gly	Val	Val	Tyr	Tyr	Val	Gly	Asp	Thr	290	295	300	
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Asn	Val	Glu	Asp	Asp	Tyr	Ile	Ala	Asn	Leu	Arg	Asn	Asn	Cys	Trp	320	325	330	
Lys	Glu	Lys	Gln	Gln	Lys	Glu	Gly	Leu	Leu	Tyr	Arg	Ala	Arg	Tyr	335	340	345	
Phe	Gly	Asp	Thr	Asp	Met	Tyr	His	Arg	Ala	Gln	Lys	Met	Gly	Thr	350	355	360	
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 Ser Glu Asp Pro Pro Asp Glu Leu Gly Pro Pro Leu Ala Glu Arg  
 50 55 60  
 Ala Leu Arg Val Lys Ala Val Lys Leu Glu Lys Glu Val Gln Asp  
 65 70 75  
 Leu Thr Val Arg Tyr Gln Arg Ala Ile Ala Asp Cys Glu Asn Ile  
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 Arg Arg Arg Thr Gln Arg Cys Val Glu Asp Ala Lys Ile Phe Gly  
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 Ile Gln Ser Phe Cys Lys Asp Leu Val Glu Val Ala Asp Ile Leu  
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 Glu Lys Thr Thr Glu Cys Ile Ser Glu Glu Ser Glu Pro Glu Asp  
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 Gln Lys Leu Thr Leu Glu Lys Val Phe Arg Gly Leu Leu Leu Leu  
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 Glu Ala Lys Leu Lys Ser Val Phe Ala Lys His Gly Leu Glu Lys  
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Lys	Glu	Val	Ala	Glu	Ala	Tyr	Glu	Val	Leu	Ser	Asp	Pro	Lys	Lys	
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Arg	Glu	Ile	Tyr	Asp	Gln	Phe	Gly	Glu	Glu	Gly	Leu	Lys	Gly	Gly	
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Ala	Gly	Gly	Thr	Asp	Gly	Gln	Gly	Gly	Thr	Phe	Arg	Tyr	Thr	Phe	
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His	Gly	Asp	Pro	His	Ala	Thr	Phe	Ala	Ala	Phe	Phe	Gly	Gly	Ser	
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Asn	Pro	Phe	Glu	Ile	Phe	Phe	Gly	Arg	Arg	Met	Gly	Gly	Gly	Arg	
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Asp	Ser	Glu	Glu	Met	Glu	Ile	Asp	Gly	Asp	Pro	Phe	Ser	Ala	Phe	
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Pro	Ser	Arg	Leu	Lys	Gln	Asp	Pro	Pro	Val	Ile	His	Glu	Leu	Arg	
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Val	Ser	Leu	Glu	Glu	Ile	Tyr	Ser	Gly	Cys	Thr	Lys	Arg	Met	Lys	
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Ile	Ser	Arg	Lys	Arg	Leu	Asn	Ala	Asp	Gly	Arg	Ser	Tyr	Arg	Ser	
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Glu	Asp	Lys	Ile	Leu	Thr	Ile	Glu	Ile	Lys	Lys	Gly	Trp	Lys	Glu	
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Gly	Thr	Lys	Ile	Thr	Phe	Pro	Arg	Glu	Gly	Asp	Glu	Thr	Pro	Asn	
				215						220					225
Ser	Ile	Pro	Ala	Asp	Ile	Val	Phe	Ile	Ile	Lys	Asp	Lys	Asp	His	
				230						235					240
Pro	Lys	Phe	Lys	Arg	Asp	Gly	Ser	Asn	Ile	Ile	Tyr	Thr	Ala	Lys	
				245						250					255
Ile	Ser	Leu	Arg	Glu	Ala	Leu	Cys	Gly	Cys	Ser	Ile	Asn	Val	Pro	
				260						265					270
Thr	Leu	Asp	Gly	Arg	Asn	Ile	Pro	Met	Ser	Val	Asn	Asp	Ile	Val	
				275						280					285
Lys	Pro	Gly	Met	Arg	Arg	Arg	Ile	Ile	Gly	Tyr	Gly	Leu	Pro	Phe	
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Pro	Lys	Lys	Ser												

&lt;210&gt; 5

&lt;211&gt; 570

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: 1977820CD1

&lt;400&gt; 5

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				20					25					30	
Arg	Ile	Val	Thr	Ser	Cys	Tyr	Gly	Pro	Ser	Gly	Arg	Leu	Lys	Gln	

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Leu His Asn Gly	Phe Gly Gly Tyr Val	Cys Thr Thr Ser Gln Ser			
	50	55			60
Ser Ala Leu Leu	Ser His Leu Leu Val	Thr His Pro Ile Leu Lys			
	65	70			75
Ile Leu Thr Ala	Ser Ile Gln Asn His Val	Ser Ser Phe Ser Asp			
	80	85			90
Cys Gly Leu Phe	Thr Ala Ile Leu Cys	Cys Asn Leu Ile Glu Asn			
	95	100			105
Val Gln Arg Leu	Gly Leu Thr Pro Thr	Thr Val Ile Arg Leu Asn			
	110	115			120
Lys His Leu Leu	Ser Leu Cys Ile Ser	Tyr Leu Lys Ser Glu Thr			
	125	130			135
Cys Gly Cys Arg	Ile Pro Val Asp Phe	Ser Ser Thr Gln Ile Leu			
	140	145			150
Leu Cys Leu Val	Arg Ser Ile Leu Thr	Ser Lys Pro Ala Cys Met			
	155	160			165
Leu Thr Arg Lys	Glu Thr Glu His Val	Ser Ala Leu Ile Leu Arg			
	170	175			180
Ala Phe Leu Leu	Thr Ile Pro Glu Asn	Ala Glu Gly His Ile Ile			
	185	190			195
Leu Gly Lys Ser	Leu Ile Val Pro Leu	Lys Gly Gln Arg Val Ile			
	200	205			210
Asp Ser Thr Val	Leu Pro Gly Ile Leu	Ile Glu Met Ser Glu Val			
	215	220			225
Gln Leu Met Arg	Leu Leu Pro Ile Lys	Lys Ser Thr Ala Leu Lys			
	230	235			240
Val Ala Leu Phe	Cys Thr Thr Leu Ser	Gly Asp Thr Ser Asp Thr			
	245	250			255
Gly Glu Gly Thr	Val Val Val Ser Tyr	Gly Val Ser Leu Glu Asn			
	260	265			270
Ala Val Leu Asp	Gln Leu Leu Asn Leu	Gly Arg Gln Leu Ile Ser			
	275	280			285
Asp His Val Asp	Leu Val Leu Cys Gln	Lys Val Ile His Pro Ser			
	290	295			300
Leu Lys Gln Phe	Leu Asn Met His Arg	Ile Ile Ala Ile Asp Arg			
	305	310			315
Ile Gly Val Thr	Leu Met Glu Pro Leu	Thr Lys Met Thr Gly Thr			
	320	325			330
Gln Pro Ile Gly	Ser Leu Gly Ser Ile	Cys Pro Asn Ser Tyr Gly			
	335	340			345
Ser Val Lys Asp	Val Cys Thr Ala Lys	Phe Gly Ser Lys His Phe			
	350	355			360
Phe His Leu Ile	Pro Asn Glu Ala Thr	Ile Cys Ser Leu Leu Leu			
	365	370			375
Cys Asn Arg Asn	Asp Thr Ala Trp Asp	Glu Leu Lys Leu Thr Cys			
	380	385			390
Gln Thr Ala Leu	His Val Leu Gln Leu	Thr Leu Lys Glu Pro Trp			
	395	400			405
Ala Leu Leu Gly	Gly Gly Cys Thr Glu	Thr His Leu Ala Ala Tyr			
	410	415			420
Ile Arg His Lys	Thr His Asn Asp Pro	Glu Ser Ile Leu Lys Asp			
	425	430			435
Asp Glu Cys Thr	Gln Thr Glu Leu Gln	Leu Ile Ala Glu Ala Phe			
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Cys	Ser	Ala	Leu	Glu	Ser	Val	Val	Gly	Ser	Leu	Glu	His	Asp	Gly
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Gly	Glu	Ile	Leu	Thr	Asp	Met	Lys	Tyr	Gly	His	Leu	Trp	Ser	Val
				470					475					480
Gln	Ala	Asp	Ser	Pro	Cys	Val	Ala	Asn	Trp	Pro	Asp	Leu	Leu	Ser
				485					490					495
Gln	Cys	Gly	Cys	Gly	Leu	Tyr	Asn	Ser	Gln	Glu	Glu	Leu	Asn	Trp
				500					505					510
Ser	Phe	Leu	Arg	Ser	Thr	Arg	Arg	Pro	Phe	Val	Pro	Gln	Ser	Cys
				515					520					525
Leu	Pro	His	Glu	Ala	Val	Gly	Ser	Ala	Ser	Asn	Leu	Thr	Leu	Asp
				530					535					540
Cys	Leu	Thr	Ala	Lys	Leu	Ser	Gly	Leu	Gln	Val	Ala	Val	Glu	Thr
				545					550					555
Ala	Asn	Leu	Ile	Leu	Asp	Leu	Ser	Tyr	Val	Ile	Glu	Asp	Lys	Asn
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&lt;210&gt; 6

&lt;211&gt; 559

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: 2722589CD1

&lt;400&gt; 6

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Tyr	Ser	Leu	Leu	Asn	Val	Arg	Arg	Glu	Ala	Ser	Ser	Glu	Glu	Leu
				20					25					30
Lys	Ala	Ala	Tyr	Arg	Arg	Leu	Cys	Met	Leu	Tyr	His	Pro	Asp	Lys
				35					40					45
His	Arg	Asp	Pro	Glu	Leu	Lys	Ser	Gln	Ala	Glu	Arg	Leu	Phe	Asn
				50					55					60
Leu	Val	His	Gln	Ala	Tyr	Glu	Val	Leu	Ser	Asp	Pro	Gln	Thr	Arg
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Ala	Ile	Tyr	Asp	Ile	Tyr	Gly	Lys	Arg	Gly	Leu	Glu	Met	Glu	Gly
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Trp	Glu	Val	Val	Glu	Arg	Arg	Arg	Thr	Pro	Ala	Glu	Ile	Arg	Glu
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Glu	Phe	Glu	Arg	Leu	Gln	Arg	Glu	Arg	Glu	Glu	Arg	Arg	Leu	Gln
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Gln	Arg	Thr	Asn	Pro	Lys	Gly	Thr	Ile	Ser	Val	Gly	Val	Asp	Ala
				125					130					135
Thr	Asp	Leu	Phe	Asp	Arg	Tyr	Asp	Glu	Glu	Tyr	Glu	Asp	Val	Ser
				140					145					150
Gly	Ser	Ser	Phe	Pro	Gln	Ile	Glu	Ile	Asn	Lys	Met	His	Ile	Ser
				155					160					165
Gln	Ser	Ile	Glu	Ala	Pro	Leu	Thr	Ala	Thr	Asp	Thr	Ala	Ile	Leu
				170					175					180
Ser	Gly	Ser	Leu	Ser	Thr	Gln	Asn	Gly	Asn	Gly	Gly	Gly	Ser	Ile
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Asn	Phe	Ala	Leu	Arg	Arg	Val	Thr	Ser	Ala	Lys	Gly	Trp	Gly	Glu

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Cys Ala Leu Gln	Phe Ser Ser Arg Gly	Ile Arg Pro Gly Leu	Thr		
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Thr Val Leu Ala	Arg Asn Leu Asp Lys	Asn Thr Val Gly Tyr	Leu		
	260		265		270
Gln Trp Arg Trp	Gly Ile Gln Ser Ala	Met Asn Thr Ser Ile	Val		
	275		280		285
Arg Asp Thr Lys	Thr Ser His Phe Thr	Val Ala Leu Gln Leu	Gly		
	290		295		300
Ile Pro His Ser	Phe Ala Leu Ile Ser	Tyr Gln His Lys Phe	Gln		
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Asp Asp Asp Gln	Thr Arg Val Lys Gly	Ser Leu Lys Ala Gly	Phe		
	320		325		330
Phe Gly Thr Val	Val Glu Tyr Gly Ala	Glu Arg Lys Ile Ser	Arg		
	335		340		345
His Ser Val Leu	Gly Ala Ala Val Ser	Val Gly Val Pro Gln	Gly		
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Val Ser Leu Lys	Val Lys Leu Asn Arg	Ala Ser Gln Thr Tyr	Phe		
	365		370		375
Phe Pro Ile His	Leu Thr Asp Gln Leu	Leu Pro Ser Ala Met	Phe		
	380		385		390
Tyr Ala Thr Val	Gly Pro Leu Val Val	Tyr Phe Ala Met His	Arg		
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Leu Ile Ile Lys	Pro Tyr Leu Arg Ala	Gln Lys Glu Lys Glu	Leu		
	410		415		420
Glu Lys Gln Arg	Glu Ser Ala Ala Thr	Asp Val Leu Gln Lys	Lys		
	425		430		435
Gln Glu Ala Glu	Ser Ala Val Arg Leu	Met Gln Glu Ser Val	Arg		
	440		445		450
Arg Ile Ile Glu	Ala Glu Glu Ser Arg	Met Gly Leu Ile Ile	Val		
	455		460		465
Asn Ala Trp Tyr	Gly Lys Phe Val Asn	Asp Lys Ser Arg Lys	Ser		
	470		475		480
Glu Lys Val Lys	Val Ile Asp Val Thr	Val Pro Leu Gln Cys	Leu		
	485		490		495
Val Lys Asp Ser	Lys Leu Ile Leu Thr	Glu Ala Ser Lys Ala	Gly		
	500		505		510
Leu Pro Gly Phe	Tyr Asp Pro Cys Val	Gly Glu Glu Lys Asn	Leu		
	515		520		525
Lys Val Leu Tyr	Gln Phe Arg Gly Val	Leu His Gln Val Met	Val		
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Leu Asp Ser Glu	Ala Leu Arg Ile Pro	Lys Gln Ser His Arg	Ile		
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Asp Thr Asp Gly					

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&lt;211&gt; 776

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;223&gt; Incyte ID No: 3658451CB1

&lt;400&gt; 9

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Asn	Arg	Phe	Phe	Glu	Met	Lys	Met	Lys	Tyr	Asp	Glu	Ser	Asp	Asn	260	265	270
Val	Leu	Ile	Arg	Ala	Ser	Arg	Ala	Leu	Thr	Asp	Lys	Val	Thr	Asp	275	280	285
Leu	Leu	Gly	Gly	Leu	Phe	Ser	Lys	Thr	Glu	Met	Ser	Glu	Val	Leu	290	295	300
Thr	Glu	Ile	Leu	Arg	Val	Asp	Pro	Thr	Phe	Asp	Lys	Asp	His	Phe	305	310	315
Leu	His	Gln	Cys	Glu	Thr	Asp	Ile	Ile	Pro	Asn	Ile	Leu	Glu	Ala	320	325	330
Met	Ile	Ser	Gly	Glu	Leu	Asp	Ile	Leu	Lys	Asp	Trp	Cys	Tyr	Glu	335	340	345
Ala	Thr	Tyr	Ser	Gln	Leu	Ala	His	Pro	Ile	Gln	Gln	Ala	Lys	Ala	350	355	360
Leu	Gly	Phe	Gln	Phe	His	Ser	Arg	Ile	Leu	Asp	Ile	Ser	Asn	Val	365	370	375
Asp	Leu	Ala	Met	Gly	Lys	Met	Met	Glu	Gln	Gly	Pro	Val	Leu	Ile	380	385	390
Val	Thr	Phe	Gln	Ala	Gln	Val	Val	Met	Val	Ile	Lys	Asn	Ser	Lys	395	400	405
Gly	Glu	Val	Tyr	Asp	Gly	Asp	Pro	Asp	Lys	Val	Gln	Arg	Met	Leu	410	415	420
Tyr	Val	Trp	Ala	Leu	Cys	Arg	Asp	Gln	Glu	Glu	Leu	Asn	Pro	Tyr	425	430	435
Ala	Ala	Trp	Arg	Leu	Leu	Asp	Ile	Ser	Ala	Ser	Ser	Thr	Glu	Gln	440	445	450
Ile	Leu																

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                   20                  25                  30  
 Ser Thr Ala Thr Gln Arg Thr Ala Gly Glu Asp Cys Ser Ser Glu  
                   35                  40                  45  
 Asp Pro Pro Asp Gly Leu Gly Pro Ser Leu Ala Glu Gln Ala Leu  
                   50                  55                  60  
 Arg Leu Lys Ala Val Lys Leu Glu Lys Glu Val Gln Asp Leu Thr  
                   65                  70                  75  
 Leu Arg Tyr Gln Arg Ala Val Ala Asp Cys Glu Asn Ile Arg Arg  
                   80                  85                  90  
 Arg Thr Gln Arg Cys Val Glu Asp Ala Lys Ile Phe Gly Ile Gln  
                   95                  100                 105  
 Ser Phe Cys Lys Asp Leu Val Glu Val Ala Asp Ile Leu Glu Lys  
                  110                 115                 120  
 Thr Ala Lys Cys Cys Ser Glu Gly Ala Glu Pro Glu Asp His Arg  
                  125                 130                 135  
 Arg Thr Leu Glu Lys Val Phe Gln Gly Leu Ser Leu Leu Glu Ala  
                  140                 145                 150  
 Arg Leu Lys Ser Val Phe Thr Lys His Gly Leu Glu Lys Met Thr  
                  155                 160                 165  
 Pro Ile Gly Asp Lys Tyr Asp Pro His Glu His Glu Leu Ile Cys  
                  170                 175                 180  
 His Met Pro Ala Gly Val Gly Val Gln Pro Gly Thr Val Ala Leu  
                  185                 190                 195  
 Val Arg Gln Asp Gly Tyr Lys Leu His Gly Arg Thr Ile Arg Leu  
                  200                 205                 210  
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Tyr His Pro Asp Lys Asn Lys Glu Pro Gly Ala Glu Glu Lys Phe					
	35		40		45
Lys Glu Ile Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Arg Lys					
	50		55		60
Arg Glu Ile Phe Asp Arg Tyr Gly Glu Glu Gly Leu Lys Gly Ser					
	65		70		75
Gly Pro Ser Gly Gly Ser Gly Gly Gly Ala Asn Gly Thr Ser Phe					
	80		85		90
Ser Tyr Thr Phe His Gly Asp Pro His Ala Met Phe Ala Glu Phe					
	95		100		105
Phe Gly Gly Arg Asn Pro Phe Asp Thr Phe Phe Gly Gln Arg Asn					
	110		115		120
Gly Glu Glu Gly Met Asp Ile Asp Asp Pro Phe Ser Gly Phe Pro					
	125		130		135
Met Gly Met Gly Gly Phe Thr Asn Val Asn Phe Gly Arg Ser Arg					
	140		145		150
Ser Ala Gln Glu Pro Ala Arg Lys Lys Gln Asp Pro Pro Val Thr					
	155		160		165
His Asp Leu Arg Val Ser Leu Glu Glu Ile Tyr Ser Gly Cys Thr					
	170		175		180
Lys Lys Met Lys Ile Ser His Lys Arg Leu Asn Pro Asp Gly Lys					
	185		190		195
Ser Ile Arg Asn Glu Asp Lys Ile Leu Thr Ile Glu Val Lys Lys					
	200		205		210
Gly Trp Lys Glu Gly Thr Lys Ile Thr Phe Pro Lys Glu Gly Asp					
	215		220		225
Gln Thr Ser Asn Asn Ile Pro Ala Asp Ile Val Phe Val Leu Lys					
	230		235		240
Asp Lys Pro His Asn Ile Phe Lys Arg Asp Gly Ser Asp Val Ile					
	245		250		255
Tyr Pro Ala Arg Ile Ser Leu Arg Glu Ala Leu Cys Gly Cys Thr					
	260		265		270
Val Asn Val Pro Thr Leu Asp Gly Arg Thr Ile Pro Val Val Phe					
	275		280		285
Lys Asp Val Ile Arg Pro Gly Met Arg Arg Lys Val Pro Gly Glu					
	290		295		300
Gly Leu Pro Leu Pro Lys Thr Pro Glu Lys Arg Gly Asp Leu Ile					
	305		310		315
Ile Glu Phe Glu Val Ile Phe Pro Glu Arg Ile Pro Gln Thr Ser					
	320		325		330
Arg Thr Val Leu Glu Gln Val Leu Pro Ile					
	335		340		